

Sf1 Cas9-KO Strategy

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Project Overview

Project Name

Sf1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sf1* gene. The schematic diagram is as follows:



Technical routes

- The *Sf1* gene has 15 transcripts. According to the structure of *Sf1* gene, exon3-exon13 of *Sf1*-208 (ENSMUST00000131252.7) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sf1* gene. The brief process is as follows: CRISPR/Cas9 system were m

- According to the existing MGI data, Mice heterozygous for a gene trapped allele exhibit embryonic lethality prior to E8.5. Mice heterozygous for a gene trapped allele exhibit increased incidence of chemically induced tumors.
- Transcript *Sf1*-207 may not be affected.
- The knockout region is near to the N-terminal of *Gm14966* gene and *Pygm* gene, this strategy may influence the regulatory function of the N-terminal of these genes.
- The *Sf1* gene is located on the Chr19. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Sf1 splicing factor 1 [*Mus musculus* (house mouse)]

Gene ID: 22668, updated on 29-Oct-2019

Summary

- Official Symbol** Sf1 provided by [MGI](#)
- Official Full Name** splicing factor 1 provided by [MGI](#)
- Primary source** [MGI:MGI:1095403](#)
- See related** [Ensembl:ENSMUSG00000024949](#)
- Gene type** protein coding
- RefSeq status** VALIDATED
- Organism** [Mus musculus](#)
- Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
- Also known as** BBP; MZFM; WBP4; Zfp162
- Expression** Ubiquitous expression in thymus adult (RPKM 49.7), adrenal adult (RPKM 41.6) and 28 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 19; 19 A [See Sf1 in Genome Data Viewer](#)

Exon count: 14

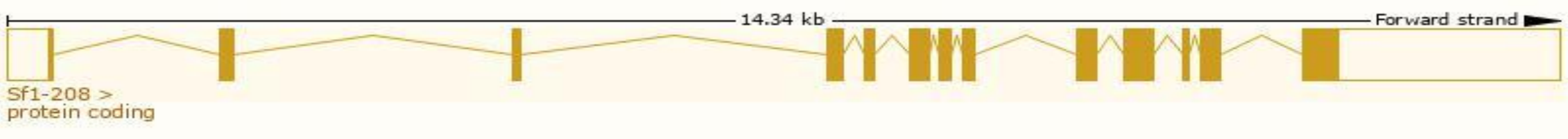
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	19	NC_000085.6 (6363673..6378038)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	19	NC_000085.5 (6363690..6378038)

Transcript information (Ensembl)

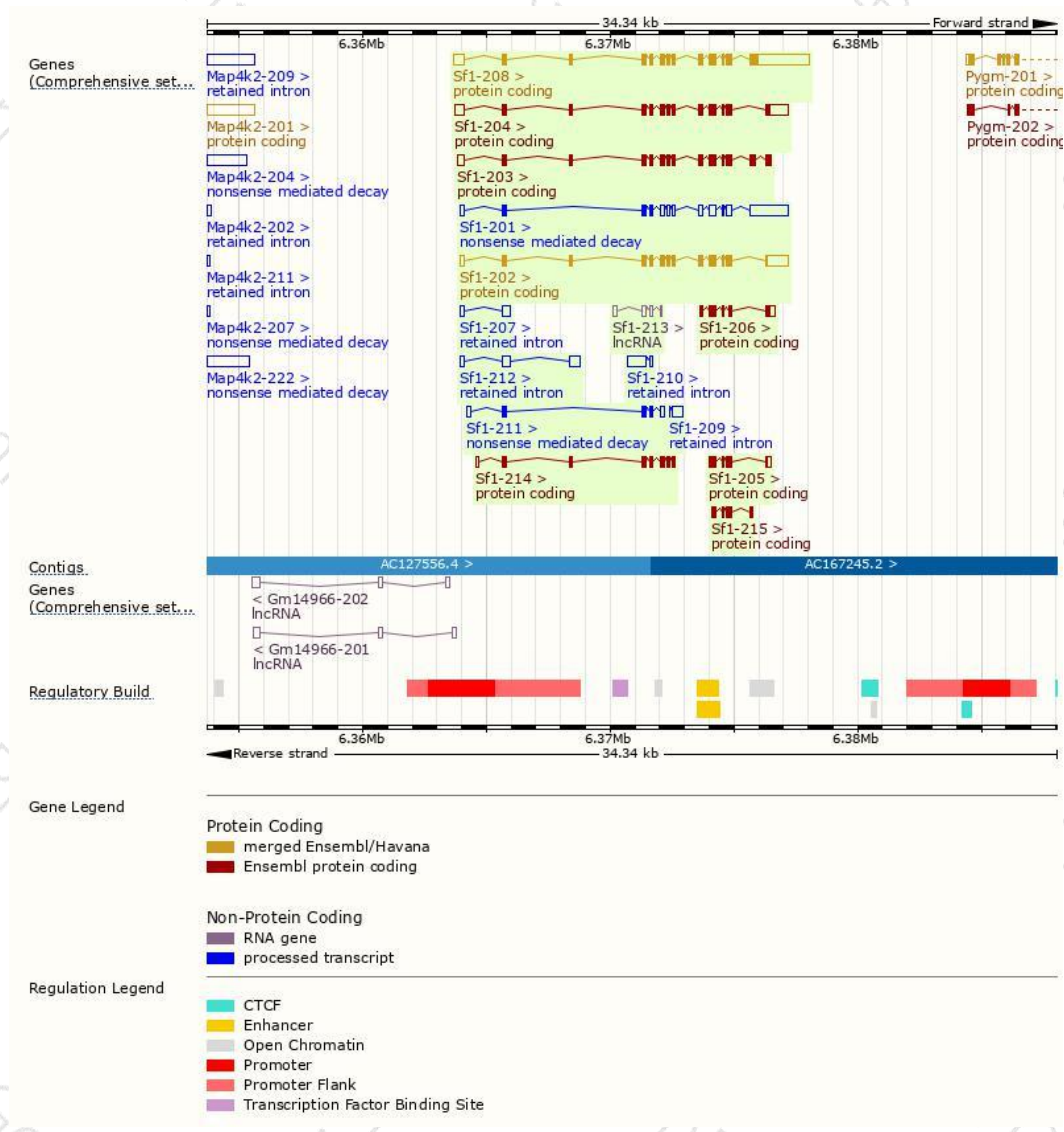
The gene has 15 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sf1-208	ENSMUST00000131252.7	4353	639aa	Protein coding	CCDS50368	Q3UI45 Q64213	TSL:1 GENCODE basic APPRIS P4
Sf1-202	ENSMUST00000113487.7	2649	548aa	Protein coding	CCDS50369	E9Q4Q2	TSL:1 GENCODE basic APPRIS ALT1
Sf1-204	ENSMUST00000113489.7	2863	571aa	Protein coding	-	D3YZC9	TSL:5 GENCODE basic APPRIS ALT1
Sf1-203	ENSMUST00000113488.7	2282	638aa	Protein coding	-	D3YZD0	TSL:5 GENCODE basic APPRIS ALT1
Sf1-214	ENSMUST00000155973.1	1000	267aa	Protein coding	-	D3YVH4	CDS 3' incomplete TSL:5
Sf1-206	ENSMUST00000125516.7	905	225aa	Protein coding	-	F6YR19	CDS 5' incomplete TSL:3
Sf1-205	ENSMUST00000124667.1	755	200aa	Protein coding	-	F6Z9W2	CDS 5' incomplete TSL:5
Sf1-215	ENSMUST00000162237.1	513	171aa	Protein coding	-	F6SRV1	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Sf1-201	ENSMUST00000113485.8	3221	110aa	Nonsense mediated decay	-	F8WHF9	TSL:1
Sf1-211	ENSMUST00000144409.7	718	84aa	Nonsense mediated decay	-	D6RDB7	TSL:3
Sf1-212	ENSMUST00000146298.1	869	No protein	Retained intron	-	-	TSL:5
Sf1-210	ENSMUST00000144239.1	785	No protein	Retained intron	-	-	TSL:3
Sf1-207	ENSMUST00000131083.7	489	No protein	Retained intron	-	-	TSL:2
Sf1-209	ENSMUST00000131677.1	408	No protein	Retained intron	-	-	TSL:3
Sf1-213	ENSMUST00000154260.1	455	No protein	lncRNA	-	-	TSL:5

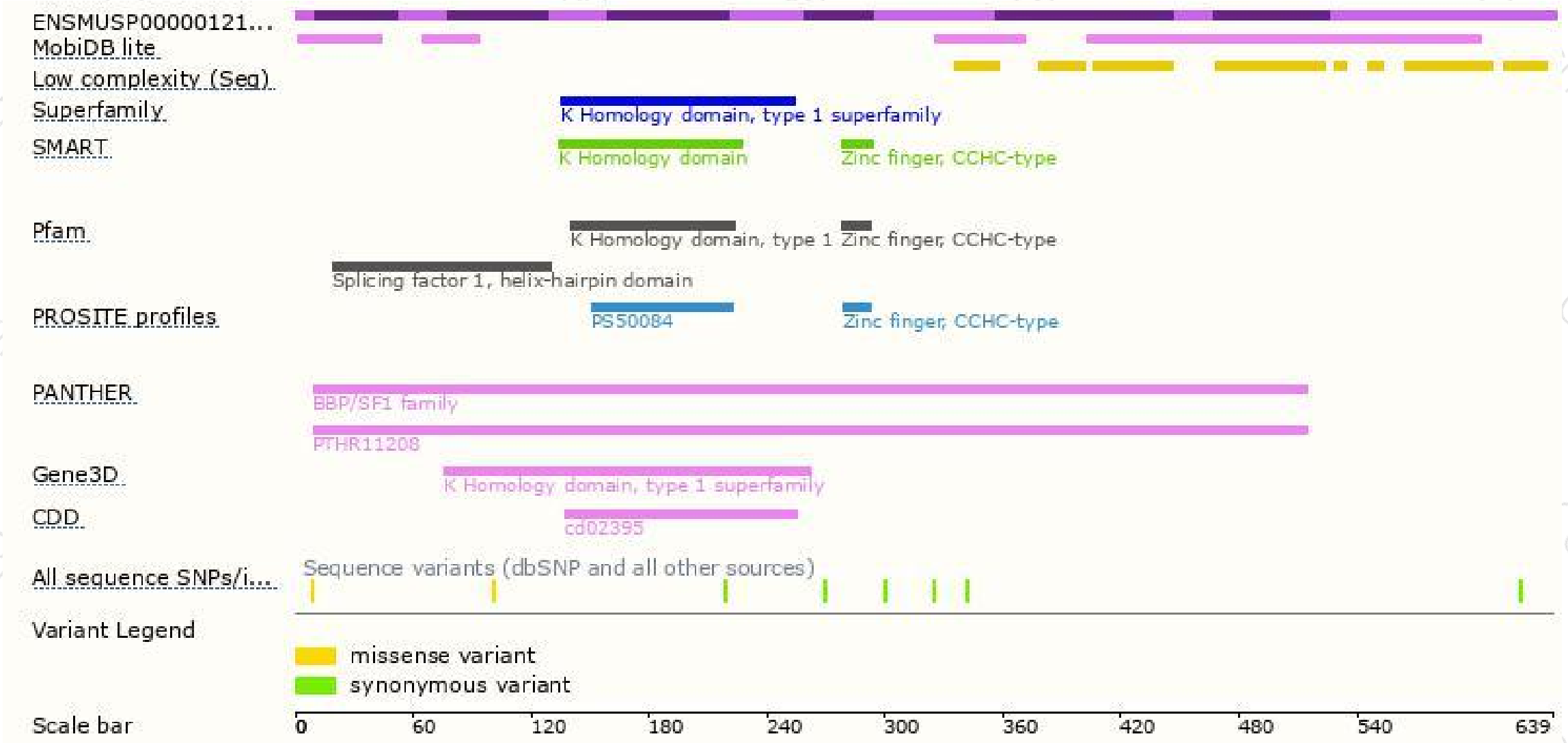
The strategy is based on the design of *Sf1-208* transcript,The transcription is shown below



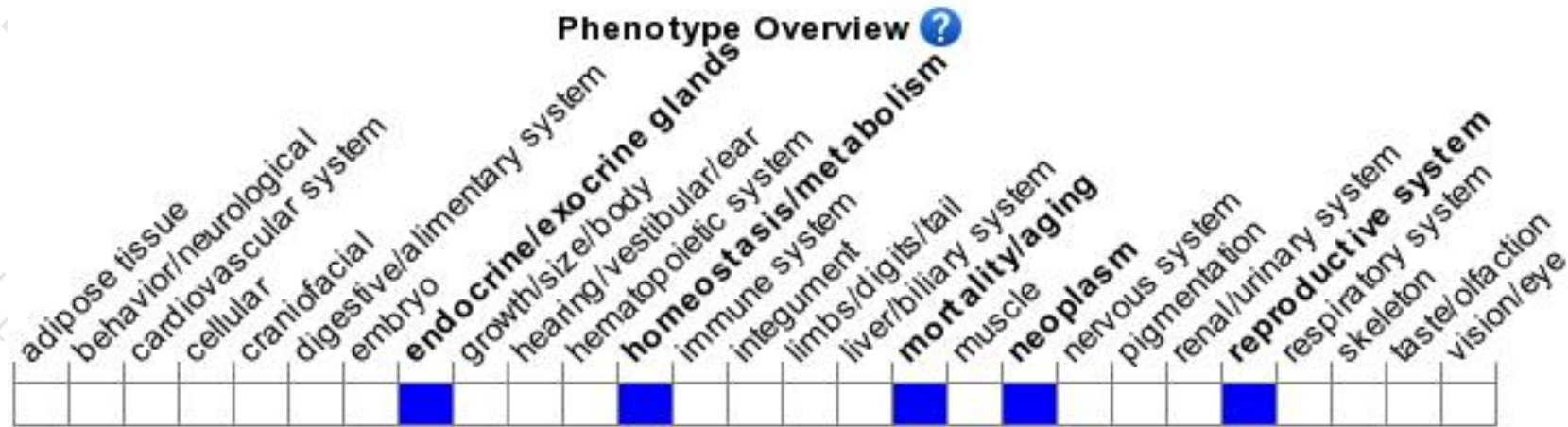
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

According to the existing MGI data, Mice heterozygous for a gene trapped allele exhibit embryonic lethality prior to E8.5. Mice heterozygous for a gene trapped allele exhibit increased incidence of chemically induced tumors.

If you have any questions, you are welcome to inquire.

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